Mycorrhizal Quantification for Prairie Chronosequence



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Introduction

- Arbuscular mycorrhizal fungi (AMF) form symbiotic relationships with a variety of plants
- Mycorrhizal roots are those which have a symbiotic relationship with fungi in the soil
- Despite their importance, few studies show the amount of external hyphae that are present in the soil (Sylvia 1992; Miller and Jastrow 1994)

Methods for Quantifying AMF Abundance

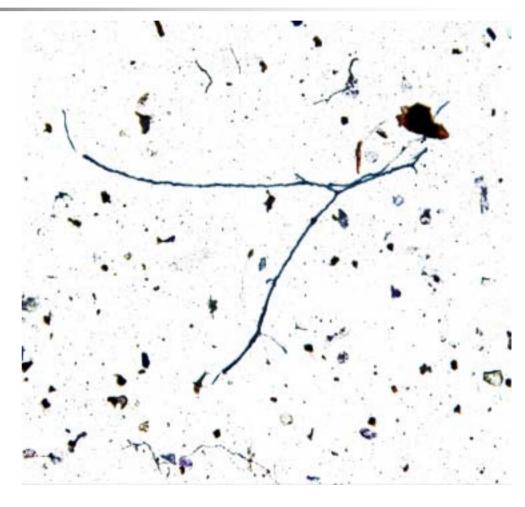
- Fatty Acid Analysis
- Hyphal Extraction
- Colonization

Fatty Acid Analysis

- Lipids extracted from freeze-dried soil and roots in a single-phase mixture of chloroform, methanol and water
- Phospholipids (PLFAs) separated from other lipid fractions using silicic acid column chromatography
- Fatty acids quantified and identified by a simultaneously run qualitative standard
- Signature for AMF is 16:1w5c

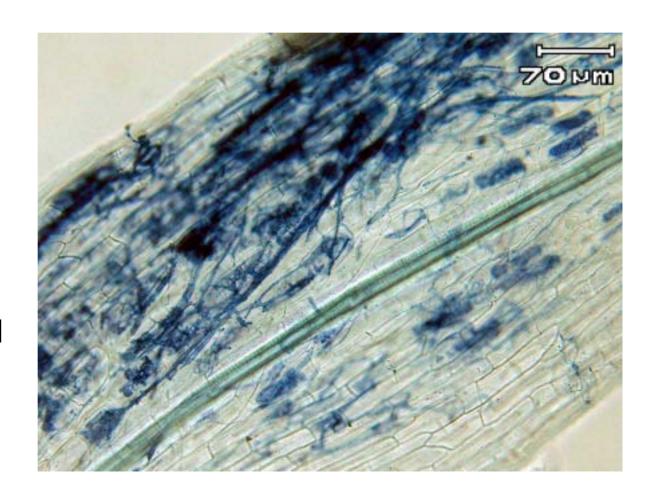
Hyphal Extraction

- Soils diluted and sonicated to break up aggregates
- Centrifuged to separate out heavier organic matter
- Stained in Trypan blue
- Filtered onto a white cellulose nitrate filter
- Quantified by visual scoring on a grid



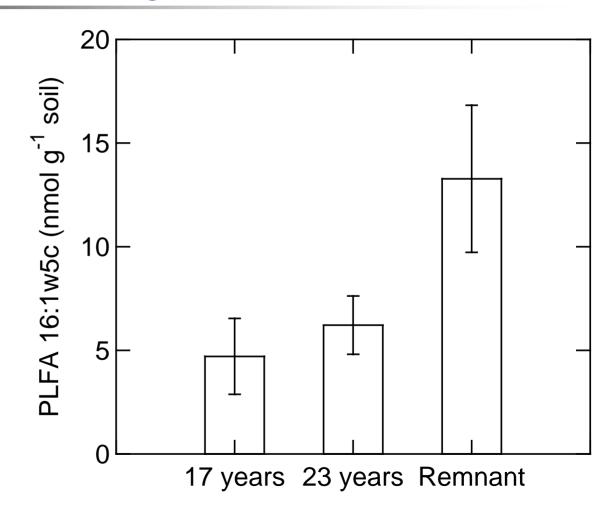
Colonization

Root colonization determined by scoring slides with roots based on the fungal structures present (coils, hyphae etc.) and the percentage of cover.

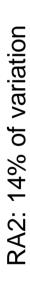


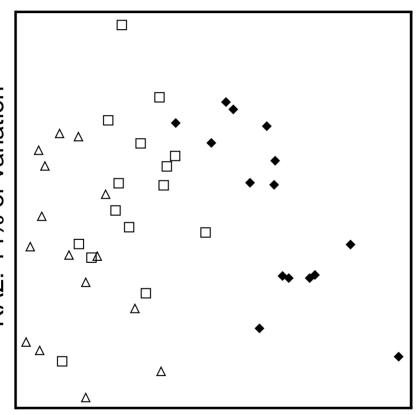
Previous Study

Previous studies showed increase in AMF with prairie succession using fatty acid analysis









- △ Restored, 17 years
- □ Restored, 23 years
- ◆ Remnant

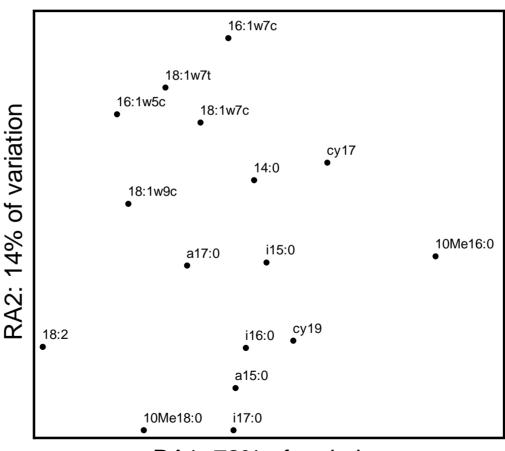
Position depends on relative abundance of 15 different fatty acids

RA1: 72% of variation



Fatty Acid Composition

Most abundant area for each fatty acid



RA1: 72% of variation

Question

Is fatty acid analysis a valid method for identifying fungal biomass present in a community?



Alternative Methods Used

- Hyphal Extraction
- Colonization

Samples

- Collected from the National
 Environmental
 Research Park at
 Fermi National
 Accelerator Laboratory
- Soil cores were taken to a depth of 10cm



Samples

- Samples were taken from:
 - 17 year post reconstruction plot
 - 23 year post reconstruction plot
 - Remnant prairie plot



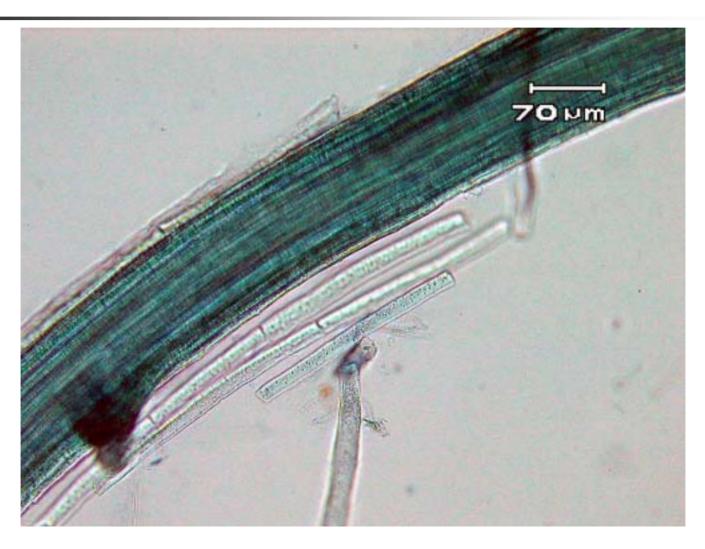


- Roots are cleared by soaking in KOH solution
 - Over cleared roots may disintegrate
 - Under cleared roots have cell contents which obscure mycorrhizal structures

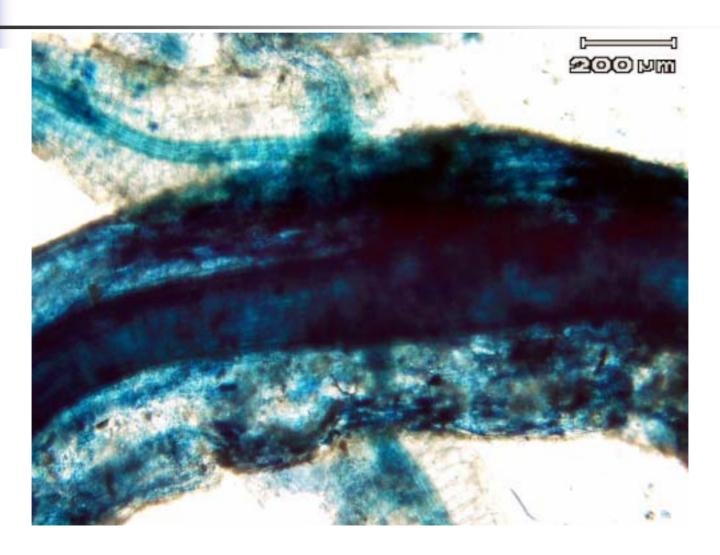
Time variances

- Fine roots need less time than thicker, tougher roots
- Root mixtures had a variety of species
- Roots removed from KOH based on appearance

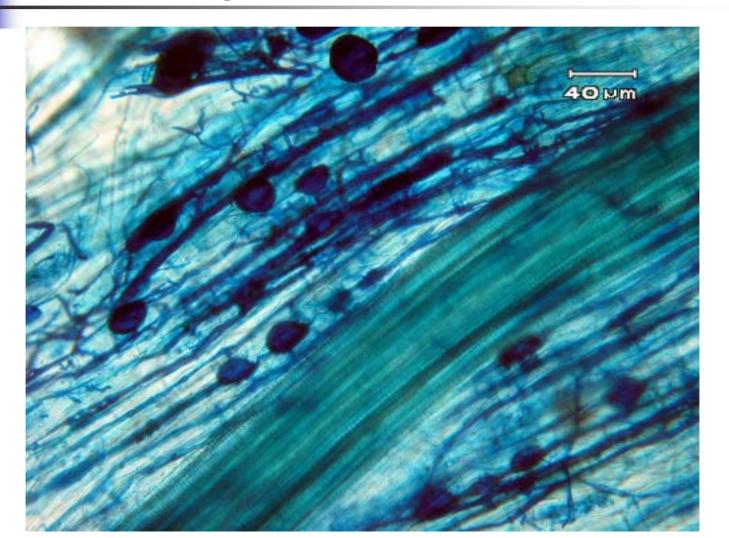
Over Cleared



Under Cleared



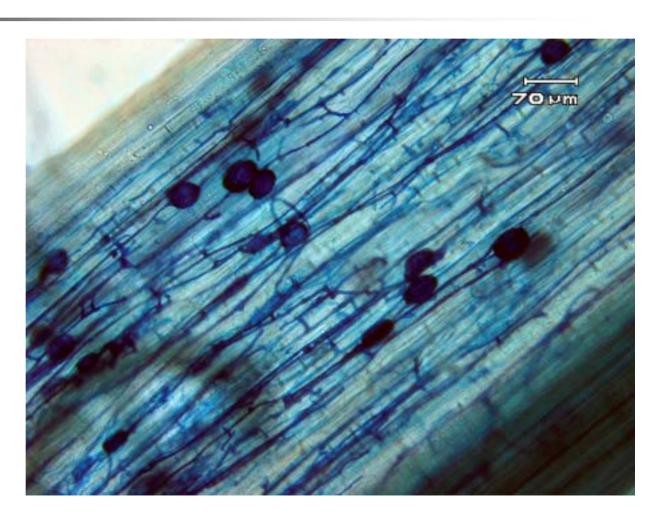
Correctly Cleared





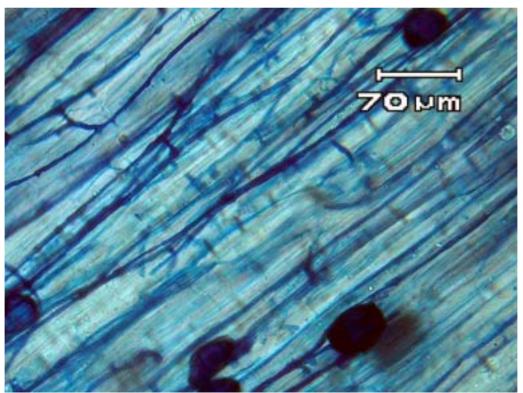
Structures for Colonization

- Hyphae
- Vesicles
- Coils
- Arbuscules





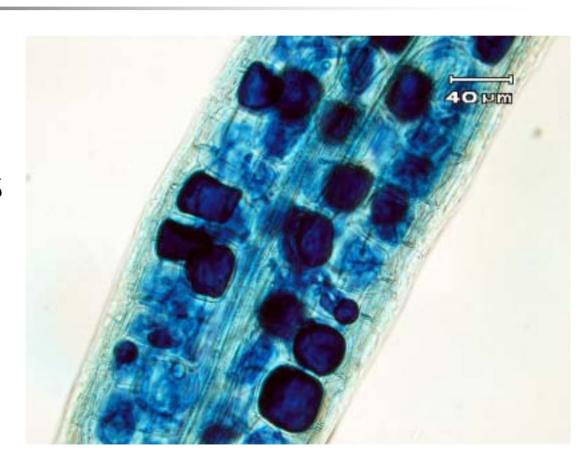
 Filamentous bodies that branch out and increase total root surface area



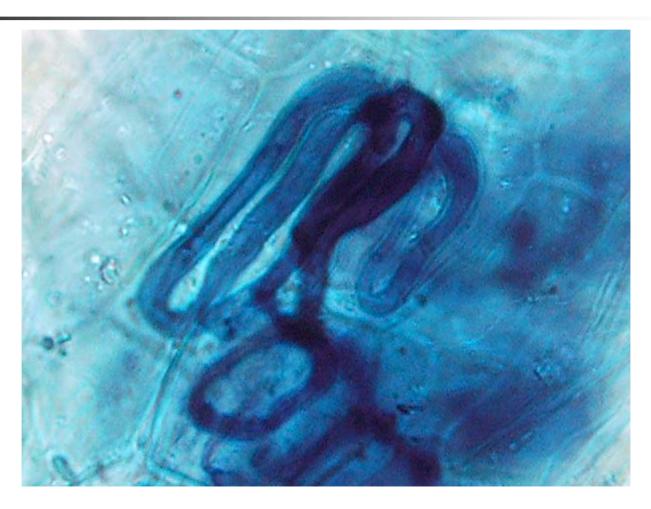


Vesicles

 Vesicles are hyphal swellings that are utilized for storage



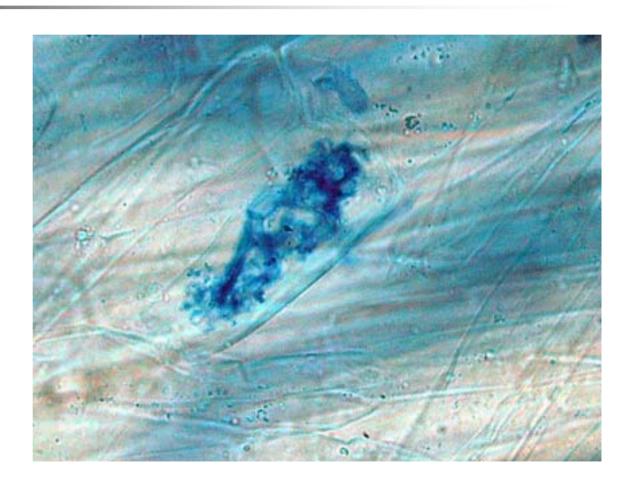
Coils





Arbuscules

 Not always present, but the main distinguishing feature for AMF fungi

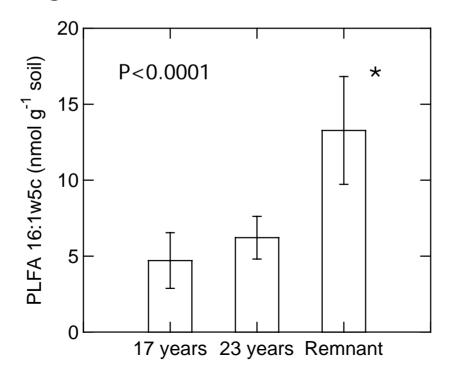


Results

Quantified and analyzed for percent infection and hyphal length.

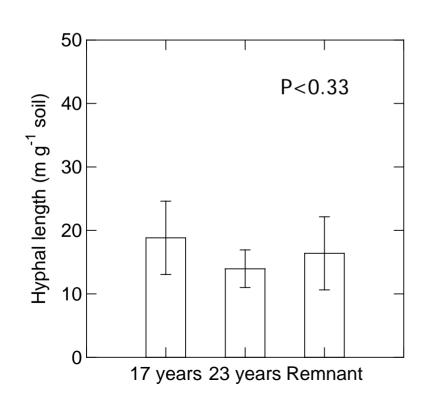
Results

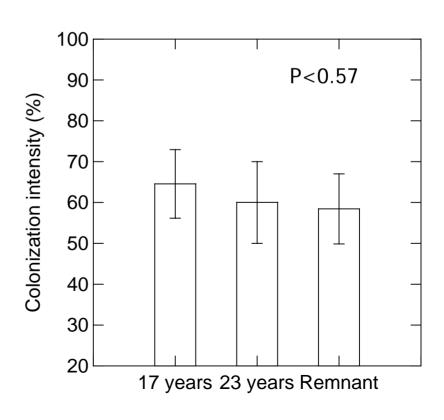
- We hypothesized that our results would correspond to the phospholipid fatty acid analysis
 - Significant differences in site



Our results

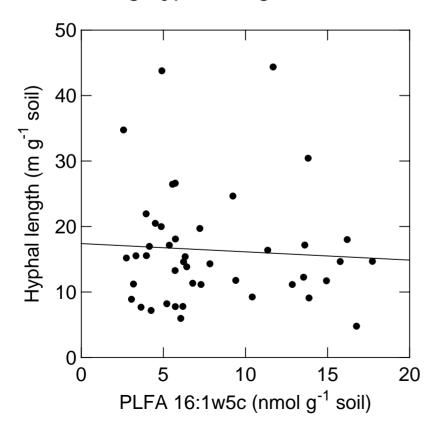
No significant differences in site

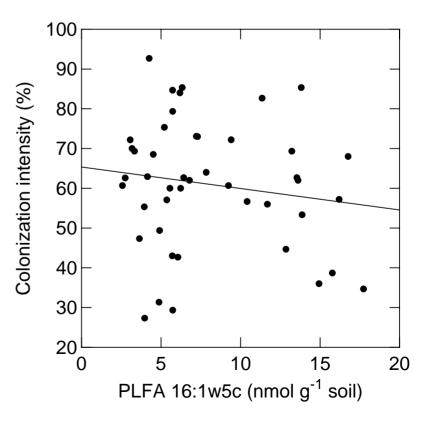




Comparison of the Two Studies

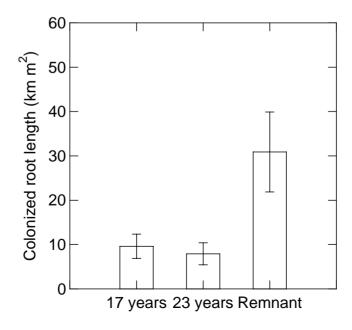
Is there a relationship between AMF measured using fatty acid 16:1w5c and using hyphal length and colonization?





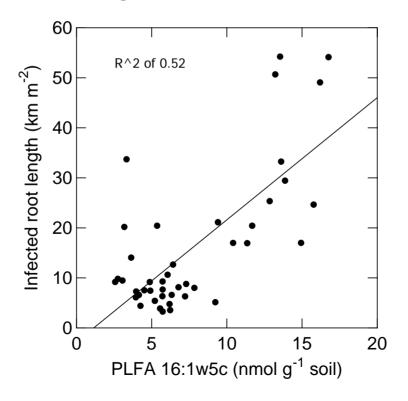


- Perhaps the fatty acid analysis results more to do with total colonized root than just percent infection.
- How does colonized root length vary with site?



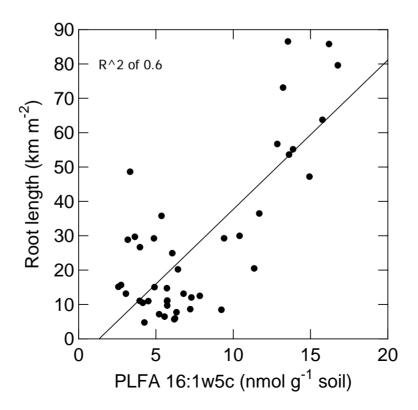
Analysis

Is there a linear relationship between AMF assessed using fatty acid, and colonized root length?



Analysis

BUT Maybe the relationship has nothing to do with our measures for colonization? Maybe the relationship is just as strong when only root length is considered?



Relationship?

- Our relationship is actually weakened when we consider percent root colonized and fatty acid analysis vs. root length and fatty acid analysis.
 - R^2 of 0.52 for % colonized
 - R^2 of 0.6 for root length

Possible Errors

- The fatty acid analysis counted living biomass only while the hyphal extraction and colonization counted both living and dead
- Extraction efficiency
 - Significantly more biomass in remnant prairie
 - Root fragments not included in samples
- Aging sonicator
- Centrifuge settings



 A follow up on extraction efficiency is being conducted



Acknowledgments

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